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Title:
Perfect score:
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
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6: geneseqp2033s:*
7: geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Query   Description	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	2	1	No.	Result
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Query Match

100.0%; Score 1788; DB 4; Length 346;

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	les the protein and co kotriene C4 receptor. Is that can be used in inflammatory disorders ulcerative colitis, a human LTC4 receptor	Japanese.	protein for ng allergic a sthma.		Matsumoto M, Saito T, I	LTD.	σ.	5.				receptor; LTC4; allergy;	NO: 2.			346 AA.	ALIGNMENTS	ABU11904	AAE02492	AAW85047	AAM25841 ADO29276	AAB85095	ADO29278	ABU11963 AAB73098	AAB85097 ABU11962	AAG77964 ABU11900	AAB85094	AAE07539 ABU11939	AAE08553
	coding sequences of a xr. These sequences can be in the treatment and ars including dermatitis, asthma and bronchitis.		screening modifiers of ligand nd inflammatory disorders, such		Sugimoto T, Ota T;							•						Abull904 Human cys	Human	Human A huma	Ado29276 Mouse GPC	Aab85095 Rat cysLT	Ado29278 Mouse GPC	Abul1963 Human HGP Aab73098 Pig LTC4	Abull962 Human HGP	Abull900 Human G-p	5094	07539	53 Human

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  08-FEB-2000;

08-FEB-2000;

09-FEB-2000;

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09-FEB-2000;

17-FEB-2000;

17-FEB-2000;

20-UTL-2000;

20-UTL-2000;

26-UTL-2000;
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/label= Signal_peptide
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/label= Mature_human_GPCR1a_protein_variant
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Matches 346;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           valve diseases, tuberous sclerosis, scleroderma, obseity, valve diseases, tuberous sclerosis, scleroderma, obseity, transplantation, adrenoleucodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host disease, acquired immune deficiency syndrome (AIDS), bronchial asthma, Crohn's disease, multiple sclerosis, and treatment of Albright Hereditary Osteodystrophy. GPCRX antibodies are used to treat a pathological state and treat or prevent disorders such as diabetes, metabolic disturbances associated with obseity, metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, infectious disease, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's disease, parkinson's disorder, immune disorders, haematopoietic disorders and various dyslipidaemias. GPCRX DNA is also useful in gene therapy. The present sequence is human GPCRIA protein
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Casman S, E
Mezes PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPCRX sequences are used to treat or prevent a human suffering from GPCR -associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosis, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful treating or preventing, e.g., cardiomyopathy, atherosclerosis, hypertension, acquired immune deficiency syndrome, bronchial ast Crohn's disease, and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-497077/54.
N-PSDB; AAD13709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human G-protein coupled receptor proteins 1-7 (GPCR1-7 or GPCRX) and nucleic acid molecules encoding such proteins
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NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV
                                                                                                                                                                       NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
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                        NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV
                                                                                              SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                                  NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                                          SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                                                                                                                                                                                           YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
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Ballinger
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ilarity 100.0%;
Conservative (
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Vernet CAM,
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Pred. No. 2.7e-180;
Mismatches 0;
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Li L, Spytek
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CA, Andrew
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RESULT 3 AAU07294

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CC disorder which is responsive to cysteinyl leukotriene receptor condulation, such as asthma, chronic obstructive pulmonary disease (COPD), altergic rhinitis, cardiac arrhythmia, myocardial ischaemia, cardiac arrhythmia, myocardial ischaemia, cardiac arrhythmia, myocardial ischaemia, alterosclerosis and heart failure. It is also useful in the therapeutic constancy disease, receptor conditions and heart failure. It is also useful in the therapeutic constancy syndrome (AIDS), rheumatoid arthritis, multiple sclerosis, considerate such as acquired immune constancy. The constancy syndrome (AIDS), rheumatoid arthritis, multiple sclerosis, converted the constancy bowel disease, systemic lupus erythematosus, inflammatory bowel disease, systemic lupus activities of cerythematosus, inflammatory bowel disease, encephalomyelitis, psoriasis, constituted dermatitis, septic shock, stroke and ischaemia reperfusion injury. The antibody to cysteinyl leukotriene receptor is useful for immunoprecipitation techniques, as tools to further elucidate the culticin of HIPHUM0000007 or its variant, and as therapeutic agent. The mucleic acid is useful for identifying mutations in HIPHUM0000007 gene culticated in human disorders, which is in turn useful for diagnosing the consistency of the disorders. It is also useful in hybridisation studies to monitor up- or down-regulation of HIPHUM0000007 expression
                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 346
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the amino acid sequence of cysteinyl leukotriene receptor polypeptide, termed as HIPHUM0000007. The nucleic acid is useful for identifying a substance that modulates cysteinyl leukotriene receptor
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Pred. No. 2.7e-180;
; Mismatches 0;
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                                                                                                                                                                                                                                                                          Domain
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                                               14-MAR-2000; 2000US-0189045P
                                                                   13-MAR-2001;
                                                                                       20-SEP-2001.
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                                                                     2001WO-EP002785
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/note= "transmembrane
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note= "transmembrane
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AC AAU0
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KW Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPCR) that has 7 transmembrane regions. Homology searches showed this creceptor to be homologous to cysteinyl leukotriene (cycl71 LTD4) receptor and P2Y receptors. The invention provides P2Y-like GPCR polypeptides and polynucleotides, expression vectors, host cells, methods for detecting the polynucleotides, methods of screening for agents which regulate or decrease the activity of a P2Y-like GPCR protein, and a pharmaceutical composition comprising an expression vector containing a P2Y-like GPCR colynucleotide or a reagent that modulates a P2Y-like GPCR polypeptide or polynucleotide. The pharmaceutical composition is used to modulate the cativity of a P2Y-like GPCR in a disease, especially a bacterial, fungal, protozoan or viral infection, pain, cancer, anorexia, bulimia, chronic obstructive pulmonary disease, asthma, Parkinson's disease, acute heart cangina pectoris, myocardial infarction, ulcer, allegy, multiple consist, benign prostatic hypertrophy, a psychotic disorder, neurological disorder and dyskinesia (all claimed)
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 346 AA;
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N-PSDB; AAH26608.
                   Homo sapiens
                                                        inverse agonist;
                                                                     Human; G-protein coupled receptor; GPCR; hRUP14; agonist;
                                                                                                                                                   23-OCT-2001
                                                                                                                                                                                                                          AAU04368 standard;
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                                                                                                            G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346;
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                                                                                                                                                 (first entry)
                                                                                                            coupled receptor, hRUP14
                                                    lung cancer.
                                                                                                                                                                                                                          protein;
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Pred. No. 2.7e-180;
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Best Local :
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23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
11-FEB-2000;
14-MAR-2000;
14-MAR-2000;
10-APR-2000;
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12-JUN-2000;
21-AUG-2000;
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10-APR-2000;
28-APR-2000;
12-MAY-2000;
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17-NOV-1999;
17-NOV-1999;
                                                                                                                                                                                                                                                                                                         hRUP14. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents.
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N-PSDB; AAS07941.
                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a human G-protein coupled receptor (GPCR), hRUP14. The endogenous and non-endogenous, constitutively activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Page 100-101; 160pp; English.
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NGSVTSCLELNLYKIAKLQTMYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
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                                                              NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                             NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                                                                       YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
                                                                                                                                                              MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
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                                                                                                                                                                                                                    100.0%; Score 1788; DB 4; ilarity 100.0%; Pred. No. 2.7e-180; Conservative 0; Mismatches 0;
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2000US-0203630P.
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2000US-0210982P.
2000US-0226760P.
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2000US-0235418P.
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2000US-0196078P.
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06-APR-2000; 2000US-01995155P.
20-APR-2000; 2000US-0199084P.
28-APR-2000; 2000US-0200551P.
05-MAY-2000; 2000US-0202278P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; neurological disorder; Huntington's disease; Parkinson's disease; cardiovascular disorder; atherosclerosis; congestive heart failure; gastrointestinal disorder; gastritis; nause; autoimmune; anamai; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; metabolic disorder; diabetes; obesity; viral infection; drug screening; chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
The present sequence is a human G-protein coupled receptor, GCREC-1 protein. The GCRECs are used for treating or preventing disorders associated with decreased expression of functional GCREC, and for
                                                                                                                                                                                                                                                                                                                                                Nguyen
Walia N
                                                                                                                                                          New human G-protein coupled receptors, useful for treatment and diagnosis of e.g. cell proliferation, also screening for specific modulators, and related nucleic acid.
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N-PSDB; AAD19577.
                                                                                                                                                                                                                                                                                                                                                                                               Policky JL,
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                                                                                                                                                                                                                                                                                                                             I DB,
                                                                                                        Page 101-102; 111pp; English.
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Lal P, Au-
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Au-Young J, Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc identifying specific agonists and antagonists, also binding agents and modulators. They can also be used for generating specific antibodies and comproteosome analysis. Disorders that can be treated include cell proliferative disorders, e.g., arteriosclerosis and cancer, neurological disorders, e.g., Huntington's disease and Parkinson's disease, cardiovascular disorders, e.g., gastricts and congestive heart failure, gastrointestinal disorders, e.g., gastricts and nausea, cardiomune/inflammatory disorders, e.g., gastricts and nausea, cardiomune/inflammatory disorders, e.g., gastricts and nausea, cardiomune/inflammatory disorders, e.g., gastricts and congestive heart failure, gastrointestinal disorders, e.g., disbetes and cobselty and viral infections. Nucleic acids that encode GCREC are used for identifying agents that alter its expression, for assessing toxicity conditions to the sources of primers and probes for diagnostic detection of GCREC DNA and of therapeutic antisense and ribozyme sequences. They can also be used in gene therapy, for chromosomal mapping, and for recombinant production of GCREC. The antibodies are useful for diagnosis and monitoring of diseases associated with GCREC expression, for detecting and purifying GCREC, and as therapeutic agents of cardiomated with GCREC and for drug screening
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                        NPILLYYFAGENFKDRIKSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
                                                                                                          SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                                                                              NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                                                                                                                                                                                                        NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                                                                                                                                                                                                                                                     NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                                                                                                                                                                                                                                                                                                          YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
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NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV
                                                                                    SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                                                      NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
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Pred. No. 2.7e-180;
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RESULT 7
AAE17231
   Human; CysIT2 GPCR; G-protein coupled receptor; cedema; asthma; immunological disorder; vascular disorder; reproductive disease; cellular metabolism; growth; development; blood; bone homeostasis; inflammation; allergy; angiogenesis; respiratory distress syndrome;
                                                                                                          inflammation; allergy; angiogenesis; respiratory distress syndrome; Crohn's disease; blood pressure; protein therapy; anti-inflammatory;
                                                                                                                                                                                                                                   07-MAY-2002
                                                                      Homo sapiens
                                                                                                                                                                                                    Human CysLT2 GPCR (G-protein coupled receptor).
                                                                                                                                                                                                                                                                AAE17231;
                                                                                                                                                                                                                                                                                           AAE17231 standard;
 Modified-site
                           Domain
                                                                                                 inflammatory
                                                                                                   disorder.
                                                                                                                                                                                                                                   (first entry)
1. .41
/label= Extracellular_domain
20. .22
                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                          protein;
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Matches 346;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing, preventing and treating inflammatory, immunological, vascular disorders, reproductive diseases, or diseases related to cellular metabolism, growth, development, blood and bone homeostasis. These disorders or diseases include asthma, inflammation, allergy, angiogenesis, respiratory distress syndrome, Crohn's disease, oedema, high or low blood pressure growth, development, blood and bone homeostasis. Human CysLT2 GPCR is also used in protein therapy. The present sequence is human CysLT2 GPCR protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide and its corresponding nucleic acid. The human CysLT2 GPCR, antibodies and compositions are useful for treating the human or animal body, or for diagnosing a disease. Human CysLT2 GPCR is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New HUMAN CYBLT2 GPCR (G-protein coupled receptor), useful for diagnosing, preventing and treating inflammatory, immunological vascular disorders, e.g. asthma, allergy, angiogenesis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 1A-1C; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human CysLT2 GPCR (G-protein coupled receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207725P
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DB; AAD28591.
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                                                                                                                                                                                    NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                                                                                                                                                                                                                                      YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
                                                                                                                                                                                                                                                                                                                                                            MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                       NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                                                                                                                                                                                      YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
                                          NGSVTSCLELNLYKIAKLQTWNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
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                                                                                                                                                                                                                                                                                                                                                                                                                          . 100.0%;
ilarity 100.0%;
Conservative 0
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seventh transmembrane domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Extracellular domain
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Pred. No. 2.7e-180;
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RESULT 8
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The sequence represents a novel G-protein coupled receptor (GPCR), PFI-CC 017* of the invention. The PFI-017 has cytostatic, antiallergic, CC 017* of the invention. The PFI-017 has cytostatic, antiallergic, CC osteopathic, cardiovascular, and immunosuppressive activity. The CC osteopathic, cardiovascular, and immunosuppressive activity. The polymucleotides may have a use in gene therapy. The polymucleotide is useful for treating allergic disorders, an inflammatory disorder, an infectious disease, an cc immunological disorder, a pulmonary disorder, an infectious disease, a neoplastic or myeloproliferative disease, or a heart disease. The cc allergic disorder is an allergic rhinitis or asthma, the pulmonary disease is COPD, and the inflammatory disorder is inflammatory bowel disease. PFI-017 polymucleotide sequences may be used for the diagnostis of disease. PFI-017 polymucleotide sequences may be used for the diagnostis of PPI-017 activity may be implicated. The polypeptides are used to produce anti-PPI-017 antibodies to be used diagnostically to detect and quantify PPI-017 antibodies to be used diagnostically to detect and quantify PPI-017 produce in disease states. The antibodies, compounds and cc compositions which can modulate the peptide can be used in treating obesity, diabetes and metabolic disease, neurological disease, urogenital disease, inflammation, cancer, osteoporosis, cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; Osteopathic; cardiovascular; immunosuppressive; neoplastic; gene therapy; heart disease; gastrointestinal disease; sleep disorder; immunological disorder; pulmonary disorder; infectious disease; myeloproliterative disease; allergic rhinitis; asthma; COPD; obesity; chronic obstructive pulmonary disease; inflammatory bowel disease; diabetes; metabolic disease; neurological disease; urogenital disease; inflammation; cancer; osteoporosis; cardiovascular disease; infection; allergy; respiratory disease; sensory organ disorder; hair loss; immunological disorder; pulmonary disease; neoplastic disease; immunological disorder; pulmonary disease; neoplastic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Fig 7B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myeloproliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PFI-017 protein and polynucleotide encoding the protein, useful diagnosing or treating metabolic diseases, urogenital disease, immunological disorders, infectious diseases, , neoplastic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harland L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2000;
19-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001; 2001US-00826791.
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antiallergic; osteopathic; cardiovascular; immunosuppressive; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human G-protein coupled receptor PFI-017*.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; GPCR; G prodrug development;
                                              Database global search for G protein-coupled receptors, encoded genes for studying in vivo signal transduction identifying targets for drug development.
                                                                                                                                                                                                                                                                                                                                     04-AUG-2000;
13-FEB-2001;
                                                                                                                                                                                   WPI; 2002-304118/34.
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2001JP-00034434.
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Pred. No. 2.7e-180;
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ABG66684 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 346 AA;
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protein;
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30-AUG-2002 (first entry)

Human novel polypeptide #19

Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; tendon; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder; fibrosis; autoimmune disorder; bacterial infection; allergic condition fungal infection.

sapiens.

06-JUN-2002.

30-NOV-2001; 2001WO-US047004

Claim 10; SEQ ID NO

58;

97pp + Sequence Listing;

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Matches 346
                                                                                                                                                                                                                                                     Sequence 346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 582-583; 672pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, cancer and promoting wound healing.
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V, Ujwal ML,
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Pred. No. 2.7e-180;
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RESULT 11 ABB05229

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                                                                                                                                                                                                                                                         The present sequence represents the human LTD4-like G protein-coupled receptor (GPCR) protein (I). (I) antiviral, protozoacide, analgesic, thave antifungal, antibacterial, antiviral, protozoacide, analgesic, cytostatic, cardiant, hypotensive, hypertensive, antianginal, anorectic, anti-lucer, antisethmatic, antiallergic, antimigraine, antiemetic, muscular, nootropic, anticonvulsant, immunostimulant, neuroprotective, neuroleptic, osteopathic and anti-HIV activities, and can be used in gene therapy and vaccine production. (I) and (II) can be used in diagnostic assays. They can also be used in identifying compounds that may be agonists or antagonists that are potentially useful in therapy, e.g. for treating bacterial, fungal, protozoan or viral infections (e.g. HIV-1), pain, cancers, diabetes, obesity, anorexia, acute heart failure, hypotension, hypertension, operanorexia, acute heart failure.
                                                                                                                               hypotension, hypertension, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, dementia, or severe mental retardation or dyskinesias (e.g. Huntington's disease or Gilles de la Tourette's syndrome). (I) and (II) can also be used in vaccines for inducing an immunological response in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; LTD4-like G protein-coupled receptor; LTD4-like GPCR; antifungal; antibacterial; antiviral; protozoacide; analgesic; cytostatic; cardiant; hypotensive; hypertensive; antianginal; anorectic; anti-licer; nootropic; antiasthmatic; antiallergic; antimigraine; antiemetic; anticonvulsant; immunostimulant; neuroprotective; neuroleptic; osteopathic; anti-HIV; gene therapy; vaccine; infection; pain; cancer; diabetes; obesity; anorexia; acute heart failure; hypotension; hypertension; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy; benign prostatic hypertrophy; migraine; vomiting; dementia; dyskinesia; severe mental retardation; Huntington's disease; immunological response; gilles de la Tourette's syndrome.
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 40; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New LTD4 receptor like G-protein coupled receptor polypeptide and polynucleotide, useful in diagnostic assays and in identifying agonists or antagonists for treating infections, pain, cancer, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130593/17.
N-PSDB; ABA92899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stroke, ulcers or asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2000; 2000EP-00112147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-2001; 2001WO-EP006313.
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  Score 1788; DB 5;
Pred. No. 2.7e-180;
; Mismatches 0;
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RESULT 12
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                                                                                                                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sclerosis; human.
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297. .:
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241. .2
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115. .
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41. 63
/note= "Transmembranes"
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300 240 240 180 180 120 120 60

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NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV

NMYSSIYFLTVLSVVRFLANVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ

YVELQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV MERKEMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI

YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV

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346;

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Similarity

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This sequence represents a human CysL2-like G-protein coupled receptor CC (GPCR) protein of the invention. The invention comprises the DNA and Cyprotein sequences of an isolated human CysLT2 (cysteinylleukotriene2)-CC like G protein-coupled receptor (GPCR) protein. This protein may have antibacterial, fungicide, virucide, cytostatic, anti-HIV, antianginal, CC exphroprotective, hypertensive, osteopathic, tranquillser, nootropic, anti-cc inflammatory neuroprotective, antiparkinsonian, analgesic, cardiant, CC excebroprotective, antiasthmatic, antiallergic, antiarthritic and cc antiplace of the CysLT2-like protein and is useful for treating cysLT2-like GPCR disorders. The protein and is useful for treating cysLT2-like protein and is useful for cc useful in raising specific antibodies which can block ligand binding, and care useful for treating disorders such as bacterial, fungal and viral confections and particularly those caused by human immunodeficiency (HIV) virus, cancers, anorexia, bulimia, cardiovascular diseases (e.g. acute heart failure, angina, mycardial infarction), ulcers, osteoporosis, contral and peripheral nervous system disease, a contral and peripheral nervous system disease, a contral and peripheral nervous system disease, a contral same multiple sclerosis). The coding sequence of cysLT2-like GPCR golymucleotide is useful for generating antisense coligonucleotides or ribozymes which specifically bind to mRNA transcribed companion.
  Query Match
Best Local S
Matches 346
                                                                                Sequence 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide, useful for treating peripheral or central nervous system, cardiovascular diseases and asthma, comprises the human cysteinylleukotriene2-like G protein-coupled receptor polypeptide.
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13-DEC-2000; 2000US-0254876P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Fig 9; 136pp; English.
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                    100
0; Mismatches 0;
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RESULT 13
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                      The invention relates to an isolated polypeptide (designated HGPRBMY11), CC which has a G-protein coupled receptor (GPCR) activity (also known as GPCR) and is encoded by the cDNA contained in ATCC Deposit CC GPCR14 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit CC domains, species homologues and proteins 95% similar to it. Also included are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including variants, fragments, complements and sequences 95% similar to the CC HGPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host cells expressing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5) diagnosing a pathological condition or a susceptibility to a pathological condition in a subject; (6) identifying an activity in a biological assay; (8) a process for making polynucleotide sequences encoding a gene product having altered GPCR activity; (9) a shuffled polynucleotide produced by the method of (8); and (10) screening for candidate compounds capable of binding to and/or modulating activity of a GPCR. The polypeptide or the polynucleotide is useful for preventing, treating or ameliorating a medical condition, particularly cardiovascular diseases or disorders, e.g. myocarddial infarction, congestive heart failure, arrhythmias, angina, through the compounds capable of thrombers or the creation of the compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; arteriosclerosis; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obesity; human immunodeficiency virus infection; HIV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human G-protein coupled receptor HGPRBMY11 polypeptide or polynucleotide, useful for preventing, treating or ameliorating myocardial infarction, angina, thrombosis, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000; 2000US-0249613P
21-DEC-2000; 2000US-0257611P
16-JUL-2001; 2001US-0305818P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 33; Fig 6; 444pp; English
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   hypertension).
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HGPRBMY11 polypeptide
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   or polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV
                                                                                                     SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACF
                                                                                                                                         NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
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Pred. No. 2.7e-180;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; cell regeneration-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohm's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hosticant protection; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hosticant protection; psoriasis; anxiety; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
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hypertension; ulcer.

hypotension; renal disorder;

rheumatoid arthritis; trauma;

Homo sapiens.

19-DEC-2000; 2000US-0257144P

2001WO-US050107.

(LIFE-) LIFESPAN BIOSCIENCES

Cysteinyl leukotriene-like G-protein coupled receptor; nootropic; cysTL2; nervous system disease; asthma; cardiovascular disease; infection; HIV; cancer; bulimia; hypertension; osteoporosis; urinary retention; angina pectoris; allergy; ulcer; Parkinson's disease; pain; inflammation; neuroprotective; uropathic; gene therapy; human.

Human cysteinyl leukotriene

(CysLT2) -like GPCR protein

11-MAR-2004

(first entry)

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The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or convidity for a particular GPCR. (I) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an CC antibodies. The peptides and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for detecting the CC gresence or absence of corresponding GPCRs. The antigenic peptides for CPCRs and antibodies are also useful for detecting the CC gresence or autoimmune diseases, growth-related diseases, cell CC regeneration-related diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, concert, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, concert, cardiomyopathy, chronic and acute inflammation, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABRA42521 to ABRA4869 encode CC GPCR proteins given in ABP81675 to ABB82018, which are used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 523pp; English
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Pred. No. 2.7e-180;
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Key Homo

Location/Qualifiers

sapiens

Region

New cDNA encoding a human cysteinyl leukotriene-like G-protein Coreceptor, useful for diagnosing, preventing or treating diseases peripheral or central nervous system disease, asthma, HIV or 07-APR-2000; 2000US-0195196P 11-DEC-2000; 2000US-0254867P 09-APR-2001; 2001US-00828479 WPI; 2003-787335/74. N-PSDB; ADH00944, ADH00946. Region Claim 4; SEQ ID NO 2; 57pp; cardiovascular disease. Xiao Y; Regior Regior Domain Domain Region 23-JAN-2003; US2003157541-A1 (FARB ) BAYER 2003US-00349021 គ្គ /note = Ti 249. .268 /note= /note= note = /note= /note= note = .308 .173 .268 . 223 . 221 "Transmembrane "Transmembrane "Transmembrane "Transmembrane Transmembrane Transmembrane Transmembrane English. helix' helix' helix" helix" domain domain domain

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RESULT 15 ADH00945 ID ADH00 XX ADH00945 standard; protein; 346

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The invention relates to a cDNA encoding a human cysteinyl leukotriene (CysLT) -like G-protein coupled receptor polypeptide. The composition and methods are useful in diagnosing, preventing, ameliorating or treating dysfunctions or diseases, including peripheral and central nervous system disease, asthma or cardiovascular disease. These may also be utilised in infections (e.g. viral, bacterial, fungal or protozoan), HIV, cancer, bulimia, hypertension, osteoporosis, urinary retention, angina pectoris, allergies, ulcers, Parkinson's disease, pain, inflammation, etc. The CysLTZ-like GPCR may also be used in identifying test compounds for human GPCR modulators, such as agonists and antagonists, partial agonist, inverse agonist or co-activators. The protein and fragments may be used

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                                                                                                                                                                                                                                                                                                                                                                                                                         in raising specific antibodies that can block the receptor and effectively prevent ligand binding. The invention is useful in gene therapy. The present sequence is human cysteinyl leukotriene (CysLT2)-like GPCR protein.
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121 NMYSSIYELTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ 180
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P49651 rattus norv P47900 homo sapien Q6nsp5 homo sapien Aah69996 homo sapi

Q7tmv7 Q99677 P32250

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MEDLINE=20459128; PubMed=10851239; DOI=10.1074/jbc.M003490200;
Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe
Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
Lynch K.R., Evans J.F.;
Lynch K.R., Evans J.F.;
Lynch K.R., Evans J.F.;
J. Biol. Chem. 275:30531-30536 (2000)
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MEDLINE=20545741; PubMed=11093801;
Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
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Bukaryota; Metazoa;
Mammalia; Eutheria;
Kopatz S.A., Aronstam R.S., Sharma S.V.; CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The molecular characterization and tissue distribution of the human cysteinyl leukotriene CysLT2 receptor.";
Biochem. Biophys. Res. Commun. 274:316-322(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20374466; PubMed=10913337; DOI=10.1006/bbrc.2000.3140; Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T., Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S., Furuichi K.;
                                                                                                                                                                                                                                                                                                         Civelli O.;
                                                               SEQUENCE FROM N.A.
                                                                                     FEBS Lett.
[5]
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       "Molecular cloning and characterization of a second human cysteinyl leukotriene receptor: discovery of a subtype selective agonist."; while Pharmacol. 38:1601-1608 (2000).
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RA Ainscough R. Jameida J. P., Ambrose K.D. Andrews D.T.,
RA Ainscough R. I. S. Babbage A.K., Bagguley C.L., Bailey J., Bannerjee R.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Catter N.P.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Catter N.P.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Ellington A.G., Faulkner L., Frankish N.G., Frankland J., French L.,
RA Ellington A.G., Faulkner L., Frankish N.G., Frankland J., French L.,
RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA Harley J.L., Hart B.A., Heath P.D., Howden P.J., Huckle B.J.,
RA Harley J.L., Hart B.A., Johnson C., Johnson D., Kay M., Kimberley A.M.,
RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamorniert D.A.,
RA Mashreghi-Mohammadi M., McLaren S.J., Newlors S., Leongamorniert D.A.,
RA Moore M.J.F., Nickerson T., Palmer S.J., Newnray A., Milne S.,
RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
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RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Roge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.

C -!- SUBCELLULAR LOCATION: Integral membrane protein.

C -!- TISSUB SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, spleen, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and clistifity in smooth muscle cells.
                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
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MIM; 605666; -.

GO: GO:0004974; F:leukotriene receptor activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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Ashcroft K.J., Beare
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                                                                                                                                                      NGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRV
                                                                                                                                                                                                                              YVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYV
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(Cytoplasmic (Potential).

2 (Potential).

2 (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

4 (Potential).

5 (Potential).

5 (Potential).

Cytoplasmic (Potential).

6 (Potential).
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By similarity.
N-linked (GlcNAc...)
N-linked (GlcNAc...)
N-linked (GlcNAc...)
N-linked (GlcNAc...)
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Pred. No. 16
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346
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RESULT 2
AAH69160
ID AAH6
AC AAH6
AC AAH6
DT 10-W
DT 1
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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AAH69160;
10-MAY-2004 (TrEMBLrel. 27,
10-MAY-2004 (TrEMBLrel. 27,
10-MAY-2004 (TrEMBLrel. 27,
                                                 TISSUE=Synthetic constructs;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYSLTR2.
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                    SEQUENCE FROM N.A.
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04 (TrEMBLrel. 27, Last annotation updat leukotriene receptor 2.
R.L., Feingold E.A., Grouse
                                                                                                                                                                                                                                                                                                                                                            Chordata; (Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                        Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
      L.H., Derge J.G.,
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E 17 E

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CLT2 PIG

STANDARD; PRT; 345 AA.

AC 095N03;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cysteinyl leukotriene receptor 2 (CysLTR2).

GN Name=CYSLTR2; Synonyms=CYSLT2;

Sus scrofa (Pig).

OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut

Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus

NCBL_TaxID=9823;

RN [1] _TaxID=9823;

RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., S
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Best Local :
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Submitted (APR-2004) to the
EMBL; BC069160; AAH69160.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Sim hes 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of the receptors."; Submitted (DEC-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB052662; BAB60817.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 181
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               QNGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLR
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                                                                                                                                                                               MERKLMSLLPSISLSEMEPNSTLGNHNSNRSCTTENFKREFYPIVYLVIFIWGALGNGFS
                                                                                                                                                                                           MERKFMSLOPSISVSEMEPNGTFSNNNS-RNCTIENFKREFFFIVYLIIFFWGVLGNGLS
                                                                                                                                          IYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLY
QKDNVTLCLELNSNKVTKLKTMNYVALVVGFVLPFGTLSICYLLIIRALLKVEVPESGLR
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79.3%;
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By similarity
N-linked (GlCNA
N-linked (GlCNA
N-linked (GlCNA
N-linked (GlCNA
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Pred. No. 2.7e.
25; Mismatches
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7 (Potential).
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N-linked (GlcNAc. ...) (Pol

N-linked (GlcNAc. ...) (Pol

N-linked (GlcNAc. ...) (Pol

5DlB1FB89BB95905 CRC64;
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Extracellular (Potential).
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2.7e-81;
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240

VSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANAC

299

LSHRKALITVIIALIIFLLCFLPYHVLRTLHLLEWKADKCKDRLHKAVAVTLALAAANSC

S

300

FNPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV

346

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RESULT 5
CLT2_MOUSE
ID CLT2_MOUSE
AC Q920A1;
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QRR52B
ID QRR52B
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Matches 226
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB058930, BAB86881.1; -...
MGD; MG1:1917336; Cysltr2.
GO; GO:0016020; C:membrane; IDA.
GO; GO:001631; F:cysteinyl leukotriene receptor activity; IDA.
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR004071; Gysleuk receptor.
Pfam; PF00001; 7tm_1; 1...
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Mammalia; Eutheria;
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Cysteinyl leukotriene 2
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PRINTS; PR00237; GPCRRHODOPSN
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21, Last sequence update)
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AND TISSUE
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                                                                                                                               SEQUENCE
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TRANSMEM
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DOMAIN
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PRINTS; PR01533; CYSLTRECPTR.

PRINTS; PR00237; GPCCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1;

PROSITE; PS50262; GPROTEIN_RECEP_F1 2;
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GO; GO:0016020; C:membrane; IDA.
GO; GO:0001631; F:cysteinyl leukotriene receptor activity; IDA.
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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28-FEB-2003 (Rel. 41, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation updat
Cysteinyl leukotriene receptor 2 (CysLTR2).
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Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse).
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Biol. Chem. 276:47489-47495 (2001).

FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Widely expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Score 1197; DI
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31; Mismatches
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By similarity.
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RESULT 6
CLT2 RAT
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STANDARD; PRT; 309 AA.

1D CLT2 RAT
CY24T9;
CY24T9;
CY24T9;
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CY28-FEB-2003 (Rel. 41, Last sequence update)
CY28-FEB-2004 (Rel. 45, Last annotation update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
CYSteinyl leukotriene receptor 2 (CYSLTR2) (RSBPT32).
CYSTERN Name=CYSlt2;
CYSTERN Name=CYSLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/amor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors.",
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

KAMOhara M., Takasaki J., Matsumoto M., Matsumoto S.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of the cloned rat and porcine cystei
                                                                                                                                                                                                                                                                                                             InterPro, IPR004071; Cysleuk_receptor.
InterPro, IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                   RGD; 619797;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB052661; BAB60816.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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  (See http://www.isb-sib.ch/announce/
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Best Local
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28-FEB-2003 (Rel. 41, Last sequence upda
01-CCT-2004 (Rel. 45, Last amoutation up
Cysteinyl leukotriene receptor 1 (CysLTF
Name=Cysltr1; Synonyms=Cyslt1;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
                                                               receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ data
--- FUNCTION: Receptor for cysteinyl leukotrienes
                                                                                                                  Takasaki J. Ohishi T.,
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Q924T8;
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                                                                                                     Pakasaki J., Kamohara
Dhishi T., Soga T., N
"Characterization of
                                                                                                                                       SEQUENCE
                                                                                                                                                          NCBI_TaxID=10116;
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      FUNCTION: Receptor for cysteinyl leukotrienes mediating constriction of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity). Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Matsushime H., Furuichi K.;
f cloned rat and porcine cys
                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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73.1%;
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Cytoplasmic (Potential).
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Cytoplasmic (Potential).
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Cytoplasmic (Potential).
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N-linked (GlCNAc. . .) (Potential).
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Pred. No. 2.3e-66;
6; Mismatches 57;
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                                                                                                                                                                                                                  ation update)
(CysLTR1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01533; CYSITRECPTR.
PRINTS; PR00237; GPCRHODODSN.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmen
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DOMAIN
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                     RLKSALRK-----GHPQKAKTKC 332
                                                                                                                                           SFMPYHIQRAIHLHFLHSETRSCDSVLRMQKSVVITLSLAASNCCFDFLLYFFSGGNFRR
                                                                                                                                                                                                                                     FPVQNINLVTQKKÅRFVCVGIWIFVILTSSPFLLSKSYQDEKNNTKCFEPPQDKQTKKYV
                                                                                               RL-STFRKHSLSSMTYIPKKKASLPEKGEEMC
                                                                                                                                                                 CFLPYHTLRTVHL--TTWKVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKD
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 (Rel. 41, Created)
(Rel. 41, Last sequence update)
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Extracellular (Potential).
7 (Potential).
Cytonla----
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4 (Potential).
Extracellular (Potential)
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Extracellular (Potential)
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By similarity.

N-linked (GlcNAc. . .) (Potential).

N-linked (GlcNAc. . .) (Potential).

1 281B41DF050DF8EA CRC64;
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PRINTS; PR01533; CYSLITRECPTR.

PRINTS; PR00237; GPCRRHODDPSN.

PROSITE; PS00237; G PROTEIN RECEP F1_1; FALSE NEG.

PROSITE; PS00237; G PROTEIN RECEP F1_2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takasaki J., Kamohara M., Saito T., Matsumoto M
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of cloned rat and porcine cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (Rel. 44, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLTR1).
Name=CYSLTR1; Synonyms=CYSLT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Receptor for cysteinyl leukotrienes mediating constriction of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By Similarity). Integral membrane protein.

SUMCELLULAR LOCATION: Integral membrane protein.
                                           84
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                                                                                                                                                                                          Similarity
                                                                                  DLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHP
IPR004071; Cysleuk_receptor.
IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                      340
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                                                                                                                                                                      Conservative
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172
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38986
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                                                                                                                                                                                        31.5%;
                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
By similarity.
N-linked (GlcNAc. . .) (
                                                                                                                                                                    75;
                                                                                                                                                                  Score 563; DB
Pred. No. 1.6e-
75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular (Potential).
7 (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular (Potential) 5 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (
4 (Potential)
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2 (Potentia:
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                                                                                                                                                                                                                                                                                                                                                                                                   (Potential)
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ong as its content is in no
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.6e-27;
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                                                                                                                                                                                                         Length 340;
                                                                                                                                                                                                                                                      CRC64;
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) (Potential).
) (Potential).
                                                                                                                                                                                                                                                                            (Potential)
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SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN-Czech II, TISSUE-Mammary gland;

MEDLINE-2388257, Pubmed-12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLT1 MOUSE STANDARD; PRT; 352 AA.

Q99JA4; Q9JJ71; Q9JK47;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cysteinyl leukotriene receptor 1 (CystTR1) (C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=C57BL/6; TISSUE=Trachea;
MEDLINE=21562332; PubMed=11705452; DOI=10.1016/S0006-2952(01)00774-2;
MEDLINE=21562332; PubMed=11705452; DOI=10.1016/S0006-2952(01)00774-2;
MEDLINE=21562332; PubMed=11705452; DOI=10.1016/S0006-2952(01)00774-2;
                                                                                                                                                                                                                                                                                                             Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann B.K.; "Identification of a murine cysteinyl leukotriene receptor by expression in Xenopus laevis occytes."; Biochim. Biophys. Acta 1517:455-459(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor) (LTD4 receptor)
Name=Cyslt1; Synonyms=Cyslt1, Cyslt1r;
Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                        SEQUENCE FROM I
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and functional characterization cysteinyl-leukotriene 1 (CysLT1) receptors."; Biochem. Pharmacol. 62:1193-1200(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maekawa A., Kanaoka Y., Lam B.K., Austen K.F., "Identification in mice of two isoforms of the creceptor that result from alternative splicing." Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                          Ogasawara H.,
Submitted (MA
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21240338; PubMed=11342226; DOI=10.1016/S0167-4781(00)00271-2; Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann E.K.;
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Blood,
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11226226; DOI=10.1073/pnas.041624398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313
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                                                                                                                                                                                                                          (MAY-2000)
                                                                                                                                                                                                                  , Izumi T., s
                                                                                                                                                                                                                                                                             (ISOFORM 2).
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                                                                                                                                                                                                                        Shimizu T.;
the EMBL/GenBank/DDBJ
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; Murinae; Mus
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Hinting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RR Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RR Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RR Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RR Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RR Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RR Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RR Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., P.C. Natle C.N., Receptor for Cysteinyl leukotrienes mediating CC CONSTITUTION: Receptor for Cysteinyl leukotrienes mediating CC constriction of the microvascular smooth muscle during an CC constriction of the microvascular smooth muscle during an CC inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4 C system. The rank order of affinities for the leukotrienes is LTD4 C System. The rank order of affinities for the leukotrienes is LTD4 C System. The rank order of affinities for the leukotrienes is LTD4 C System. The rank order of affinities for the leukotrienes is LTD4 C System. The rank order of affinities for the leukotrienes is LTD4 C NATERNATIVE PRODUCTS:
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2; Synonyms=Short;
ISOId=099JA4-2; Sequence=VSP_001921;
TISSUE SPECIFICITY: Widely expressed, with higher expression in the lung and skin, intermediate levels in the heart, kidney and stomach and lower levels in several other tissues. Isoform 1 is the most abundant form in all tested tissues.
MISCELLANEOUS: MK-571, a selective antagonist, was shown to inhibit eosinophilia, bronchial hyperreactivity and microvasculal leakage. Zafirlukast (Accolate) and pranlukast (Onon) were also shown to be selective antagonists.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1; Synonyms=Long;
IsoId=Q99JA4-1; Sequence=Displayed;
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Onon) were also
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EMBL; AF329272; AAK16715.1; -.
EMBL; AF329272; AAK16716.1; -.
EMBL; AF205830; AAK15433.1; -.
EMBL; AF263370; AAF73047.1; -.
EMBL; AB044087; BAA96809.1; -.
EMBL; BC027102; AAH27102.1; -.
                                                                                                                                                                           Pfam; PF00001; /LW_1, ...
PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1_2;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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GO; GO:0004974; F:leukotriene receptor activity; IDA.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
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1 (Potential).

Cytoplasmic (Potential).

2 (Potential)

Extracellular (Potential).

3 (Potential).

Cytoplasmic (Potential).

4 (Potential).

Extracellular (Potential).

5 (Potential).
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Nature
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14-APR-2004 (TrEMBLrel. 27, Created)

14-APR-2004 (TrEMBLrel. 27, Last sequence update)

14-APR-2004 (TrEMBLrel. 27, Last annotation update)

14-APR-2004 (TrEMBLrel. 27, Last annotation update)

Adult male colon cDNA, RIKEN full-length enriched library,

clone:9030217A18 product:CYSTEINYL LEUKOTRIENE 1 RECEPTOR LONG
ISOFORM, full insert sequence.
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                             SEQUENCE FROM N.A.
STRALN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
STRAILN=C2354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.", Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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N-linked (GlCNAc...) (I

N-linked (GlCNAc...) (I

Missing (In isoform 2).

/FTId=VSP 001921.

Y > D (in Ref. 3).
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7 (Potential).
Cytoplasmic (Potential).
By similarity.
N-linked (GlcNac. . .) (Potential)
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9; Mismatches
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Pred. No. 2.6e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108;
  cDNA collection.";
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; Murinae; Mus.
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EXAMPLE STRAIN-C57BL/61; TISUE=COlon;

Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

A Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W.,

Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

A Hayashida K., Hayatsu N., Hiranoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kouda M., Koya S.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Kurihara C., Matsuyama T., Miyazaki A., Ohno M., Ohsato N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayasshizaki Y.;

EL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Best Local
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Genome Res.
[6]
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MEDLINB-20530913; PubMed=11076861;
Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB=COlon;

MEDLINE=20499374, PubMed=11042159;

Carninoi P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs

prepare full-length cDNA libraries for rapid discovery of new

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=99279253; PubMed=10349636;
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                                                                                                                                                         LLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTWN
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Pred. No. 2.
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gabe Y., Tagami P
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RESULT 11
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                                                        This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                           Warren C.N., Aronstam R.S., Sharma S.V.; "CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99393629; PubMed=10462554;
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Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Mett
Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connoll
Bai C., Austin C.P., Chateauneuf A., Stocco R., Greig G.M.,
Kargman S., Hoose S.B., Hosfield E., Williams D.L. Jr.,
Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;
"Characterization of the human cysteinyl leukotriene CysLT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cystchnyl leukotriene receptor 1 (CystTR1) (CystCor) (LTD4 receptor) (HG55) (HMTMF81).
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05-JUL-2004 (Rel.
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Q9Y271;
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Mammalia; Eutheria; Primates;
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Homo sapiens (Human).
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s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outset European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for con
                                                                                                    and heart.
MISCELLANEOUS: Selective antagonists, such as montelukast
(Singulair), zafirlukast (Accolate) and pranlukast (Onon), are
used in the treatment of the asthma crisis.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed, with highest levels in spleen and peripheral blood leukocytes. Lower expression in several tissues, such as lung (mostly in smooth muscle bundles)
                                                                                                                                                                                                                                                                                                             FUNCTION: Receptor for cysteinyl leukotrienes mediating bronchoconstriction of individuals with and without asthma. Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, edema, eosinophil migration and damage to the mucus layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4
                                                                                                                                                                                                     alveolar macrophages), placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323
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EMBL; AF313266; AAD42778.1; -.
EMBL; AF33266; AAD427778.1; -.
EMBL; AY242130; AAO92297.1; -.
HSSP; P34996; IDDD.
Genew; HGNC:17451; CYSLTR1.
MIM; 300201; -.
GO; GO:0005887; C:integral to pl
GO; GO:0005887; C:integral to pl
GO; GO:000584; C:membrane fract
GO; GO:0004974; F:leukotriene re
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GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0004974; F:leukotriene receptor activity; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration
GO; GO:0005952; P:defense response; TAS.
GO; GO:0007585; P:respiratory gaseous exchange; TAS.
InterPro; IPR0004071; Cysleuk receptor.
InterPro; IPR0004276; GPCR_Rhodpsn.
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PRINTS; PR01533; CYSLTRECPTR.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; F7

PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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or send an email to license@isb-sib.ch).
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                        SALRK 322
                                                                        PYHTLRTVHLTTW--KVGLCKD-
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                                                 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL-
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38.0%;
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N-linked (GlCNAc. . .) (
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Pred. No. 2.9e-27;
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X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altachul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

X Altopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

X Raha S.S., MocWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Rahaks. M., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

X Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

X Allakosley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Allakosley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Rahakseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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Q8IV19;
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Submitted (JUL-2002)
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Reingold B.A., Grouse L.H.,
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Mammalia; Eutheria;
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InterPro; IPR000276; GPCR_Rhodpsn.
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GO:0016021; C:integral to membrane; IEA.
GO:0004974; F:leukotriene receptor activi
GO:0004872; F:receptor activity; IEA.
GO:007186; P:G-protein coupled receptor
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                                                    RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM
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Pred. No. 6.8e-27;
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SEQUENCE FROM N.A.

MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;

"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GP80_HUMAN STANDARD; PRT; 337 AA.

996F68; Q86TL1;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Probable G protein-coupled receptor GPR80 (P2Y-like receptor) (P2Y-like GPCR).

Name=GPR80; Symonyms=GPR99;
                                                                                                                                                                                                             Suwa M., Sato T., Okouchi I
Tsutsumi S., Aburatani H.,
"Genome-wide discovery and
                                                                                                                                                                                                                          [4]
SEQUENCE FROM N.A.
Seto T., Okouchi I.,
ABE
                                                                                                                                                                                                                                                                                                                                                                 Wittenberger T., Hellebrand S., Munck A., Schaller H.C., Hampe W., "GPR99, a new G protein-coupled receptor b of nucleotide receptors.", BMC Genomics 3:17-17(2002).
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                                                                                                 Submitted
                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Thyroid;
                                                                                                                                                                                     receptor genes.";
Submitted (JUL-2001)
                                                                                                                                                                                                                                                                            genome sequence.";
FEBS Lett. 520:97-101(2002).
                                                                                                                                                                                                                                                                                                   MEDLINE=22040266; PubMed=12044878;
Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku
"Identification of G protein-coupled receptor genes
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                                                                                                          receptor.
                                                                                                                       Bruess M., Bonisch "Molecular cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                               FUNCTION: Orphan receptor.
SUBCELULIAR LOCATION: Integral membrane protein.
SUBCELULIAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Detected in kidney and, to a lower extend placenta. Not detected in brain tissues including the frontal placenta. Not detected in brain tissues including the frontal placenta. Not detected in brain tissues including the frontal placenta.
          pons.
SIMILARITY:
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Yama Y.;
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EMBL; AF370886; AAM76912.1; -
EMBL; AB083598; BAB93311.1; -
EMBL; AB065877; BAC06095.1; -
EMBL; AJ305372; CAC83857.1; -
Genew; HGNC:4531; GPR80.
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PRINTS; PRO0237; G PROTEIN RECEP F1 1; FA
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000276; GPCR
InterPro; IPR002286; P2_pu
Pfam; PF00001; 7tm_1; 1.
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                                            --WYNLILTATTECLELVIVTLCYTTIIHTLTHGLQTDSCLK---QKARRLTILLLLAPY
                                                                                                                 LQTMNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF
                                                                                                                                                          RLLHVTSIRSAWILCGIIWILIMASSI---MLLDSGSEQNGS----VTSCLELNLYKIAK
                                                                                                                                                                                            NCTDENIPLKWHYLPVIYGIIFLVGFPGNAVVISTYIFKWRPWKSST---IIMLNLACTD
                                                                                                                                                                                                                                                         NCTIEN--FKREEFPIVYLIIFFWGVLGNG--LSIYVF-LQPYKKSTSVNVFMLNLAISD
                    RLKSALR---KGHPQKAK
                                                                                                                                            SCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIK---
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337
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38251
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2_purnocptor.
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                                                                                                                                                                                                                                                                                              64;
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2 (Potential).
Extracellular (Potential).
3 (Potential).
4 (Potential).
4 (Potential).
5 (Potential).
Extracellular (Potential).
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
6 (Potential).
7 (Potential).
Extracellular (Potential).
17 (Potential).
18 (Potential).
19 (Potential).
19 (Potential).
19 (Potential).
                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential)
By similarity.
N-linked (GlcNAc...)
F -> L (in Ref. 5)
F -> R (in Ref. 5)
                     329
                                                                                                                                                                                                                                                                                            Score 487.5; DB 1;
Pred. No. 8.1e-23;
4; Mismatches 114;
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                                                                                                                                                                                                                                                                                                                                           -> L (in Ref. 5).
-> R (in Ref. 5).
6814EA0044756CE6 CRC64;
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(Potential)
(Potential)
(Potential)
                                                                                                                                                                                                                                                                                                                    337;
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                                                                                                                                                                                                                                                                                             Gaps
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PRESULTY 14

PRITY HUMAN

TO 13071/2091D61, 09UE21

TO 15-JUL-2000 (Rel. 41, Lase sequence update)

TO 5-JUL-2000 (Rel. 41, Lase sequence, update)

TO 6000 (Rel. 41, Lase sequence, update)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOID-Q13304-2; Sequence=VSP_001987;
--- TISSUE SPECIFICITY: Primarily expressed in brain.
---- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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        Extracellular (Potential).

1 (Potential).

Cytoplasmic (Potential).

2 (Potential).

Extracellular (Potential).
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                                                                                                                                                               1.
1.
receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lvie A.;
primarily
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Best Local S
Matches 116
                                                                                                                                                                                                             Q8N5S7;
Q8N5S7;
01-OCT-2002
01-OCT-2002
01-MAR-2004
GPR17 protei
MEDLINE-22386257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.,
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DOMAIN
TRANSMEM
                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                TISSUE=Brain;
                                                                                                                                           SEQUENCE FROM N.A.
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Primates;
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Last sequence Last anno
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N-linked (GlcNAc. . .) (Pot
N-linked (GlcNAc. . .) (Pot
Missing (in isoform 2).
/FTId=VSP 001987.
W; 132FBE97BE83C60C CRC64;
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By similarity.
N-linked (GlcNA
N-linked (GlcNA
N-linked (GlcNA
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6 (Potential).
Extracellular (Potential)
7 (Potential)
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Pred. No. 1.3e-22;
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annotation update)
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Best Local S
Matches 115
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PRINTS; PR00237; GFCRRHODOPSN.

PRINTS; PR01157; PS2YDUNNOCPTR.

PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN_1.

PROSITE; PS00237; G PROTEIN_RECEP_F1 2; 1.

PROSITE; PS50262; G PROTEIN_RECEP_F1 2; 1.

SEQUENCE 339 AA; 37860 MW; BBÖCAFDOFC371D63 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.;
"Generation and initial analysis of
"Generation and initial analysis of
and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
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296
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|||::||::||:||:||||
PANVEIMHIAVADISCVIVLPTRIVYHESGNHWEEGEIACRITGEIEYINMYASIYEITC
MYFFVAEKFRHALCNLLCGKRLKGPPPSFEGK
                                                                                                                                      TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPL
                                                                                                                                                                                                                              NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR----KALT
                                         LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
                                                                                               MIAIVLAIFLVCFVFYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDFI
                                                                                                                                                                                            -LYR-EKASHHALVSLAVAFTFFFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 481.5;
Pred. No. 1.
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Bouffard
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A., Schein J.
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Search completed: December 13, 2004, 17:52:34 Job time: 191 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/backfIles1.pep:*
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Gapop 10.0 , Gapext 0
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1788
1 MERKFMSLQPSISVSEMEPN.....KAKTKCVFPVSVWLRKETRV 346
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    GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                    Length
    B
  US-09-585-876-2
US-09-044-404A-2
US-09-586-924-2
US-08-153-848-44
US-08-812-871-3
US-09-189-813-44
US-09-170-496D-32
PCT-US95-07180-2
US-09-170-496D-182
US-09-170-496D-182
US-09-170-496D-182
US-09-170-496D-182
US-09-170-496D-184
US-08-513-9748-374
US-08-513-9748-374
US-08-513-9748-374
US-08-513-524A-4
US-08-513-524A-4
US-08-513-678-4
US-08-513-678-4
US-09-170-496D-78
US-09-170-496D-78
US-09-170-536-954-4
US-09-170-538-4
US-09-170-538-4
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US-08-852-824-17
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US-08-852-824-17
US-08-467-947A-30
US-08-467-947A-3
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Sequence 2, Appli
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Sequence 44, Appli
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Sequence 37, Appli
Sequence 27, Appli
Sequence 182, Appli
Sequence 182, Appli
Sequence 4, Appli
Sequence 78, Appli
Sequence 17, Appli
Sequence 30, Appli
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DB Q	8 8 8 8	B & B	Query Ma Best Loo Matches Qy Db	28 39 30 31 31 31 31 32 41 33 35 36 36 36 37 37 37 37 37 37 37 37 37 37 37 37 37
301 NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVF	181 NGSVTSCLELNLYKIAKLQTMNYIALVVGCLL	<u> </u>	1tch 2al s 344 1	437 24.4 34.4 3 US 434 24.3 361 4 US 434 24.3 371 4 US 434 24.3 374 4 US 9.5 23.5 374 4 US 416 23.3 375 1 US 416 23.3 375 2 US 416 23.3 375 3 US 416 23.3 375 1 US 6.5 22.7 398 1 US 6.5 22.7 39
HPQKAKTKCVFPVSVWLRKETRV 	PFFTLS         FFTLS		99.5%; Score 1779; DB 4; Length 346; 99.4%; Pred. No. 3.7e-131; tive 1; Mismatches 1; Indels 0; Gaps ISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLS	77-947A-8 15-842-17 15-842-17 15-842-15 15-842-15 18-876-9 12-134A-2 13-9724A-3 13-972-3 14-272-2 14-272-2 14-272-2 14-272-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 16-976-6 17-9840-6 18-976-6 18-
7 346 7 346	ICYLLIIRVLLKYEVPESGLRV 240	12 18 18	1 346;  LS 0; Gaps 0;  LIIFFMGVLGNGLSI 60  LIIFFMGVLGNGLSI 60  LIIFFMGVLGNGLSI 60	Sequence 8, Appli Sequence 206, App Sequence 17, Appl Sequence 15, Appl Sequence 373, Appl Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli

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US-09-044-404A-2
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APPLICANT: SATHE, G
APPLICANT: HALSEY,
APPLICANT: ELLIS, C
APPLICANT: AMES, RC
                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 337 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                       190
                                                                                                                    130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDGKNNTKCFEPPQDNQTKNHVLVL
                                                                                                                                                      145 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 201
                      262
                                                                                 202 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 261
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                                                                                                                                                                                                                                                     10 SATCHDTIDDFRNQVYSTLYSMISVVGPFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD
                                                                                                                                                                                                                                                                         27 NSRNC--TIENPKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                          LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF
PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACENPLLYYFAGENFKDRLK 317
                                                HYVSLFVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM
                                                                                                                                                                                       LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 amino acids
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HALSEY, WENDY
ELLIS, CATHERINE
AMES, ROBERT
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SARAU, HENRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                      31.3%; Score 559; DB 3; Length 337; 38.0%; Pred. No. 3.6e-36; ative 71; Mismatches 106; Indels
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A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/09/044,404A
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SOFTWARE: PASTSEQ FOR WI
SEQ ID NO 2
LENGTH: 337
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-586-924-2
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TITLE OF INVENTION: CDAR CLONE HMTMF81 THAT ENCODES A NOVEL
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
FILE REFERENCE: GH-70001-1D1
CURRENT APPLICATION NUMBER: US/09/586,924
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1997-04-22
NUMBER: PASTARE: FASTSEQ for Windows Version 3.0
                                                                                                      RESULT 4
US-08-153-848-44
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US-09-586-924-2
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                                                  Sequence 44, Application US/08153848 Patent No. 5759804 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.3%;
Best Local Similarity 38.0%;
Matches 116; Conservative 71
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APPLICANT: SATHE,
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APPLICANT:
APPLICANT:
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                APPLICANT:
   APPLICANT:
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5. 6506878
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                                                                                                                                                                                                                                                                                                                        HYVSLFVGFIIPEVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSEM
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                                                                                                                                                                              STFRK 311
                                                                                                                                                                                                                  SALRK 322
                                                                                                                                                                                                                                                                                      PYHTLRTVHLTTW -- KVGLCKD -- RLHXALVITLALAAANACFNPLLYYFAGENFKDRLK 317
                                                                                                                                                                                                                                                                                                                                                                                             QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDGKNNTKCFEPPQDNQTKNHVLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD
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HALSEY, WENDY
ELLIS, CATHERINE E
AMES, ROBERT S.
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Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 559; DB 4; Length 337; pred. No. 3.6e-36; 71; Mismatches 106; Indels
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RESULT 5
US-08-812-871-3
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.

NAME: NO. 5759804and, Greta E.

NAME: NO. 5759804and, Greta E.
Sequence 3, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.0%;
Best Local Similarity 34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (312) 474-04
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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OGY: linear
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Bicknell
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Best Local Similarity 34.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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CITY: Palo Alto
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LIBRARY: GenBa
CLONE: 992700
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NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HI
TITLE OF INVENTION: PROTEIN
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ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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296
                                       304 LYYFAGENFKDRLKSAL----RKGHPQKAKTK 331
                                                                                                                 248 TIIITLIIFFLCFLPYHTURTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPL 303
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Muzong Cheng
NVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
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Pred. No. 2.7e-30;
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Best Local Similarity
Matches 115; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
REGISTER Uhl
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APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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LENGTH: 339 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
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PRIOR APPLICATION NUMBER: US 09/088,337
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                                        248 TIIITLIIFFLCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACENPL 303
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amino acid
NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR----KALT 247
                                                                              -LYR-EKASHHALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
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6300 Sears Tower,
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US-09-088-337B-44
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 44:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-198
CLASSIFICATION WIMBER: US 08/153,848
PELICATION NUMBER: US 08/153,848
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 35.02
REFERENCE/DOCKET NUMBER: 31794
TELEBHONE: (312) 474-6300
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
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191 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR----KALT 247
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                                                                                                                                                  65 PANVFLMHLAVADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTC
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                                                                                                                                                                              SVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTV 131
                                                                ISADRFLAIVHPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ- 183
                                                                                                                                                                                                                                    EVAPPGLITNESLATAEQCGQETPLENMLEASEYLLDEILALVGNTLALWLEIRDHKSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                     27.0%;
ilarity 34.6%;
Conservative 63
                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                     Score 483.5; DB 3;
Pred. No. 2.7e-30;
3; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1
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RESULT 9
PCT-US93-11153-44
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 339
                                     Sequence 44, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, App
Patent No. 6555
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Best Local (
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-09-170-496D-32
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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen M.
TITLE OF INVENTION: No. 6555319-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 -LYR-EKASHHALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115;
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                                                                                                                                                                                                                                                                                                                MYFFVAEKFRHALCNLLCGKRLKGPPPSFEGK 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISADRFLAIVHPVKSLKLRRPLYÄHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ- 183
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Marshall, O'Toole, Gerstein, Murray & Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%; Score 483.5; DB 4; 34.6%; Pred. No. 2.7e-30; tive 63; Mismatches 129;
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                                                                                                                            Sequence 2, Application PC/TUS9507180
GENERAL INFORMATION:
APPLICANT: LI, YI
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Matches 115;
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Best Local Similarity
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                                            APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OP INVENTION: G-PROTEIN
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                       CORRESPONDENCE ADDRESS
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CITY: C
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TELEX: 25-3856
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  ADDRESSEE:
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  CARELLA,
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BYRNE,
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  BAIN,
                                                                   RECEPTOR
  GILFILLAN, CECCHI
                                                                   HIBEB69
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ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND

COUNTRY: U

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RESULT 11
US-09-170-496D-182
; Sequence 182, Application US/09170496D
; Patent No. 6555339
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                                                                                                                                                                                             GENERAL INFORMATION:
             APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous,
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
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Best Local S
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NUMBER OF SEQ ID NOS:
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FILING DATE: 06-UNNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
AMMB: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKST NUMBER: 3258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
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SOFTWARE: PatentIn Release #1.0, ...
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: PCT/US95/07180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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115; Conserv
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US-08-513-974B-374
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SEQ ID NO 182
LENGTH: 339
TYPE: PRT
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Best Local Similarity
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                                                    PILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JE
PILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROCOMPATION:
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/513,974B
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APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Ohtaki, Shoji
APPLICANT: Ohtaki, Recorrin COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
PRIOR APPLICATION DATA
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                 APPLICATION NUMBER: FILING DATE: 19-AUG
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                 19-AUG-1995
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Pred. No. 4.6e-30;
2; Mismatches 130
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 6-
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-
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PRIOR APPLICATION DATA:
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FILING DATE: 16-MAR
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                                                                                 CFNPLLYYFAGENFKDRLKSALRK 322
                                                                                                                              ALTTIIITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANA 298
                                                                                                                                                                     TADEYLRSYFVYSMCTTVFMFCI----PPIVILGCYGLIVKALIYKDLDNSPLR---RK
                                                                                                                                                                                                                                                       VVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEONGSVTSCLE- 189
                                                                                                                                                                                                                                                                                                                                          ELLAGGWAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRFWSGI
                                                                                                                                                                                                                                                                                                                                                                     EMEPNGTFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSV 73
                                                     CVDPILYFLAGDTFRRRLSRATRK 330
                                                                                                               STYLVIIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNS
                                                                                                                                                                                              ----LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRK 244
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Pred. No. 9.5e-29;
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APPLICATION UNHER: 10/08/781,250
FILING DATE: 10-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER:
FILING DATE:
FILING DATE:
ATTORNEY/A---
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.0%; Score 447.5; DB 3; Best Local Similarity 31.6%; Pred. No. 1.9e-27; Matches 109; Conservative 74; Mismatches 141;
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APPLICANT: Sathe,
APPLICANT: Van Ho:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 370 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: William T. Han,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SmithKlir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 709 5 Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-4060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
 299
                                   293 LAAANACFNPLLYYFAGENFKD------RLKSALRKGHPQKAK 329
                                                                                                                                                180 NVNNATTTCFEGFSKRVWKTYLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLS
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                                                                                                                                                                                                                                                          120 VNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIML-LDSGS 178
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LATLNCCFDPFIYYFTLESFQKSFYINAHIRMESLFKTETPLTTK 343
                                                                                              TNIYGSMLFLTCISVDRFLAIVYPFRSRTIRTRRNSAIVCAGVWILVLSGGISASLFSTT
                                                                                                                                                                                                                                                                                                      LFVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKI-FYNFNRHWPFGDTLCKISGTAFL
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                                                                                                                                                                                                                                                                                                                                                                                                                  ERKFMSLOPSISVSEMEPN-GTFSNNNSRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLS
                                                                           QIGTNKKKVLKMITVHMAVFVVCFVPYNSVLFLYALVRSQAITNCFLERFAKIMYPITLC
                                                                                                                                                                                     EQNGSVTSCLELNLYKIAK--LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPES
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709 Swedeland
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Van Horn, Stephanie
Bergsma, Derk
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RESULT 15
US-08-559-524A-4
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US-09-745-842-14
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SEQ ID NO 14
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                    Sequence 4, Application US/08559524A Patent No. 5871963
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09745842 Patent No. 6762029 GENERAL INFORMATION:
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Best Local
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/99/745,842
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 60/171,622
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hollopeter, Gunter APPLICANT: COR Therapeutics, Inc. TITLE OF INVENTION: P2712 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                      APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEB: MORGAN, LEWIS & BOCKIUS LLP
                 STATE: D.C.
COUNTRY: US
                                                 STREET: 1800 M St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                        324 YFLAGDTFRRRLSRATRK 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 RSYFIYSMCT----TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 VVYPLKSLGRLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTIT-CYDTTSDEYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 TESNNNSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN
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20036-5869
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Jantzen, Hans-Michael
Ramakrishnan-DuBridge, Vanitha
                                                                      B: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
                   USA
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Search completed: December 13, 2004, 17:54:06 Job time : 42 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 0444
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
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                                                                                         SRATRK
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Sequence:
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1 MERKFMSLQPSISVSEMEPN.....KAKTKCVFPVSVWLRKETRV 346
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gn2_6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/USO9_NBW_PUB.pep:*
gn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                                                          2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2.6/ptodata/2/pubpaa/US61_NEW_PUB.pep:*
2.6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
2.6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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US-09-866-230-7
US-09-866-230-9
US-09-828-478-2
           US-09-779-679-2

US-09-9779-679-26

US-09-991-225-30

US-09-980-049-1

US-10-225-567A-589

US-10-349-021-2

US-10-349-021-2

US-10-321-807-14

US-10-331-332A-2

US-10-369-405-30
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Sequence 6, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 30, Appli
Sequence 1, Appli
Sequence 589, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 14, Appli
Sequence 2, Appli
Sequence 30, Appli
Sequence 30, Appli
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88 100.0 346 15 US-10-403-161-24 Sequence 100.0 346 15 US-10-343-650A-58 Sequence 100.0 346 16 US-10-321-807-14 Sequence 100.0 346 16 US-10-321-807-14 Sequence 100.0 346 16 US-10-312-807-88 Sequence 100.0 346 17 US-10-757-262-40 Sequence 100.0 346 16 US-10-318-807-88 Sequence 100.0 346 16 US-10-318-405-5 Sequence 100.0 346 16 US-10-318-405-2 Sequence 100.0 346 16 US-10-364-405-2 Sequence 100.0 346 17 US-10-364-405-2 Sequence 100.0 346 18 US-10-290-175-965-110 Sequence 100.0 346 18 US-10-290-175-356 Sequence 100.0 346 18 US-10-255-1767-547 Sequence 100.0 346 18 US-10-255-1767-547 Sequence 100.0 346 18 US-10-349-021-5 Se	15
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US-10-403-151-24 US-10-297-247-2 US-10-331-650A-58 US-10-321-607-14 US-10-321-007-88 US-10-314-048A-14 US-10-314-048A-88 US-10-314-048A-88 US-10-314-048A-88 US-10-399-405-55 US-09-826-791-2 US-10-399-405-5 US-09-826-791-2 US-10-399-405-2 US-10-399-405-2 US-10-399-78-5 US-09-826-731-5 US-09-826-731-5 US-09-826-731-5 US-09-826-731-5 US-09-826-731-5 US-09-931-25-6 US-10-349-021-5 US-10-349-021-5 US-10-349-021-5 US-10-369-405-6 US-10-369-405-6 US-10-369-405-6 US-10-369-405-6 US-10-369-405-6 US-10-369-405-6 US-10-369-405-6 US-10-400-991-6 US-10-400-991-6 US-09-933-798-4 US-09-933-798-4 US-09-885-453-1	346
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sequence sequence	10-182-605-2 10-403-161-2
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## ALIGNMENTS

RESULT 1 US-09-826-791-6

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SEQ ID NO 6
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Patent No. US20010039037A1
GENERAL INFORMATION:
                                                                                                                                                                                                                  Matches 346; Conservative
                                                                                                                                                                                                                                    Query Match 100.0%; Score 1788; DB 9 Best Local Similarity 100.0%; Pred. No. 3e-148;
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TITLE OF INVENTION: NO. US20010039037A1el Polypeptide
FILE REFERENCE: PC10914ADAM
CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
FRIOR APPLICATION NUMBER: 0008504.3
PRIOR PILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
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121 NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
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Sequence 9, Application US/09866230
Patent No. US20020150901A1
GENERAL INFORMATION:
APPLICANT: Murphy, Andrew, et al.
TITLE OP INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
FILE REPERENCE: RRG 771.A
CURRENT APPLICATION NUMBER: US/09/866,230
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APPLICANT: MUTPLY, Andrew, et al.
APPLICANT: MUTPLY, Andrew, et al.
TITLE OP INVENTION: NO. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
FILE REPERBYCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
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Best Local Similarity
Matches 346; Conserv
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 3e-148;
ative 0; Mismatches 0;
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CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 2
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                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo
US-09-828-478-2
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US-09-828-478-2
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APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Protein
FILE REFERENCE: 04974.00458
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Best Local Similarity
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/207,
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
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ORGANISM: Homo
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YVFLQPYKKSTSVNVFMINLAISDLLFISTLFFRADYYLRGSNWIFGDLACRIMSYSLYV
                                                                                 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI
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100.0%; Pred. No. 3e-148;
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                                                                                                                                 Score 1788; DB 9;
Pred. No. 3e-148;
); Mismatches 0;
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                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-679-2
                            Query Match
Best Local Similarity
Matches 346; Conserv
                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR PILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/183191
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/180,929
PRIOR FILING DATE: 2000-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Andrew, David P
APPLICANT: Mezes, Peter S
TITLE OF INVENTION: No. US20030082757A1el Proteins and Nucleic Acids
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APPLICANT: Burgess, Catherine
APPLICANT: Padigaru, Muralidh
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: USSN PRIOR FILING DATE: 2000-02-09
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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FILING DATE: 2000-07-20
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FILING DATE: 2000-02-09
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FILING DATE: 2000-07-26
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FILING DATE: 2000-02-09
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FILING DATE: 2000-07-20
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MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSI 60
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Casman, Stacie
Ballinger, Robert
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Padigaru, Muralidhara
Tchernev, Velizar T
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                                                    Score 1788;
Pred. No. 3
                                  Mismatches
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                                                  SOFTWARE: Pa
SEQ ID NO 26
LENGTH: 346
TYPE: PRT
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                 ORGANISM: Homo sapiens
                                                                                                                                   PRIOR APPLICATION NUMBER: USSN 60/219585
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181157
PRIOR FILING DATE: 2000-02-09
                                                                                                                   PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 65
                                                                  346
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PatentIn Ver.

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RESULT 6
US-09-779-679-26
PRIOR APPLICATION NUMBER: USSN 60/18191
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/183191.
PRIOR APPLICATION NUMBER: USSN 60/180,929
PRIOR APPLICATION NUMBER: USSN 60/180,929
PRIOR APPLICATION NUMBER: USSN 60/219758
PRIOR APPLICATION NUMBER: USSN 60/219758
PRIOR APPLICATION NUMBER: USSN 60/181339
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR APPLICATION NUMBER: USSN 60/21341
PRIOR APPLICATION NUMBER: USSN 60/181392
PRIOR PRICING DATE: 2000-07-26
PRIOR PRICING DATE: 2000-07-26
PRIOR PRICING DATE: 2000-07-26
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TITLE OF INVENTION: No. US20030082757A1el Proteins and
FILE REFERENCE: 15966-661
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CURRENT FILING DATE: 2001-02-08
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Casman, Stacie
Ballinger, Robert
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Padigaru, Muralidhara
Tchernev, Velizar T
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; ORGANISM: Homo sapiens
US-09-991-225-30
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US-09-991-225-30
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Best Local Simi
Matches 346;
                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1788; DB 10; Length 346; Best Local Similarity 100.0%; Pred. No. 3e-148; Matches 346; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 30 LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/09991225
Publication No. US20030153063A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED |
TITLE OF INVENTION: HEART AND VARIANTS THEREOF
FILE REFERENCE: DO075.NP
CURRENT APPLICATION NUMBER: US/09/991,225
CURRENT APPLICATION NUMBER: 60/249,613
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR PILING DATE: 2000-11-21
PRIOR PILING DATE: 2001-07-16
PRIOR PILING DATE: 2001-07-16
PRIOR PILING DATE: 2001-07-16
PRIOR PILING DATE: 2001-07-16
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   NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
                                                                                       NMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ
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APPLICANT: DAS, Debopriya

ITITLE OF INVENTION G-PROTEIN COUPLED RECEPTORS

FILE REFERENCE: PI-0072 PCT

CURRENT APPLICATION NUMBER: US/09/980,049

CURRENT FILING DATE: 2001-11-28

PRIOR APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278

PRIOR FILING DATE: 2000-03-29; 2000-04-06; 2000-04-20; 2000-04-28; 2000-05-05

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PERL Program

SEQ ID NO 1

LENGTH: 346

TYPE: PPT
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; NAME/KEY: misc_feature
; OTHER INPORMATION: Incyte ID No: 5628963CD1
US-09-980-049-1
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US-09-980-049-1
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Best Local Similarity 100.0%;
Matches 346; Conservative 0
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APPLICANT: INCYTE GENOMICS, INC.
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ORGANISM: Homo sapiens
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GRAUL, Richard
KHAN, Farrah A.
NGUYEN, Danniel B.
PATTERSON, Chandra
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Pred. No. 3e-148;
D; Mismatches O; Indels O;
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; ORGANISM: Homo sapiens
US-10-225-567A-589
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CURRENT APPLICATION NUMBER: US/10/349,021
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10349021 Publication No. US20030157541A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 589
LENGTH: 346
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TITLE OF INVENTION: Regulation of Human CysLT2-Like
TITLE OF INVENTION: Protein
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OP INVENTION; ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
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                                                                                     PRIOR APPLICATION NUMBER: US/09/714,008
PRIOR PILING DATE: 2000-11-16
PRIOR PELING DATE: 1999-11-17
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PRIOR PILING DATE: 2000-04-20
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PRIOR APPLICATION NUMBER: 60/171,900
PRIOR PILING DATE: 1999-12-23
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PRIOR PILING DATE: 1999-12-23
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US-10-321-807-14
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US-10-349-021-2
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SEQ ID NO 2
LENGTH: 346
TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 3e
Matches 346; Conservative 0; Mismatches
                         Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 133 SOPTWARE: PatentIn version 3.0
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APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: No. US20030166148A1-Endogenous,
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN0086
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CURRENT FILING DATE: 2002-12-16
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Wrapper or

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Sequence 2, Application US/1013132A

Publication No. US20030203833A1

GENERAL INFORMATION:

APPLICANT: Ignar, Diane

APPLICANT: Pillai, Sreekumar

TITLE OF INVENTION: Cysteine Leukotriene 2 Receptor Pol
FILE REFERENCE: PU4824

CURRENT APPLICATION NUMBER: US/10/131,332A

CURRENT FILING DATE: 2002-07-02

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 346

TYPE: PRT

ORGANISM: Homo sapiens

US-10-131-332A-2
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; TYPE: PRT
; ORGANISM: Homo s
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Similarity 100.0%;
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Pred. No. 3e-148;
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RESULT 14 US-10-182-605-2

Sequence 2, Application US/10182605
Publication No. US20040023861A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL PROTEIN

FILE REFERENCE: N78955A

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP
TITLE OF INVENTION: THEREOF
FILE REFERENCE: DO075A CIP
CURRENT APPLICATION NUMBER: US/10/369,405
CURRENT APPLICATION NUMBER: US. 60/249,613
PRIOR APPLICATION NUMBER: U.S. 60/249,613
PRIOR FILLING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: U.S. 09/991,225
PRIOR FILLING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: U.S. 60/257,611
PRIOR APPLICATION NUMBER: U.S. 60/257,611
PRIOR APPLICATION NUMBER: U.S. 60/257,611
PRIOR APPLICATION NUMBER: U.S. 60/305,818
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US-10-369-405-30
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                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 346;
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TYPE: PRT
ORGANISM: Homo sapiens
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NPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVFPVSVWLRKETRV
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RESULT 15
US-10-403-161-22
US-10-403-161-22
; Sequence 22, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/370349
PRIOR FILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-04-08
PRIOR PILING DATE: 2002-04-08
PRIOR PILING DATE: 2002-04-08
PRIOR PILING DATE: 2002-08-15
PRIOR PILING DATE: 2002-08-15
PRIOR PILING DATE: 2002-04-12
PRIOR PILING DATE: 2002-04-22
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PRIOR PILING DATE: 2002-09-69
PRIOR PILING DATE: 2002-09-69
PRIOR APPLICATION NUMBER: 60/379679
PRIOR APPLICATION NUMBER: 60/181045
PRIOR APPLICATION NUMBER: 60/181045
PRIOR PILING DATE: 2000-02-08
PRIOR PILING DATE: 2000-02-08
PRIOR PILING DATE: 2000-01-22
PRIOR FILING DATE: 2000-01-22
PRIOR APPLICATION NUMBER: 60/25897
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: 60/262892
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PRIOR FILING DATE: 2001-01-39
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-605-2
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Matches 346; Conserv
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CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: GB 0003079.1
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, David et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 21402-573C
CURRENT APPLICATION NUMBER: US/10/403,161
CURRENT FILING DATE: 2003-03-31
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US-10-403-161-22
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Search completed: December 13, 2004, 18:05:05
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I50241
JC4737
JC4162
B45680
T09508
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S13638
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45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	ω L	30
356.5	356.5	357	357	359	360	361.5	362.5	363	366	366.5	367.5	371.5	372	372.5	373.5
19.9	19.9	20.0	20.0	20.1	20.1	20.2	20.3	20.3	20.5	20.5	20.6	20.8	20.8	20.8	20.9
361	333	363	328	363	432	352	369	359	362	355	427	365	363	378	387
N	N	N	N	N	N	N	N	N	N	N	N	N	N	ผ	N
JC5653	I65989	A49092	JC4800	148261	A43448	A43113	JC2083	S15403	JN0694	G02436	S17148	868208	I57940	A55735	169202
G protein-coupled	G protein-coupled	angiotensin II rec	P2Y6 receptor -	angiotensin II rec	thrombin receptor	chemokine (C-C) re	somatostatin recep	angiotensin II rec	angiotensin II rec	chemokine (C-C) re	alpha-thrombin rec	G protein-coupled	somatostatin recep	G protein-coupled	G protein-coupled

## ALIGNMENTS

G protein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 66-Jun-1995 #sequence\_revision 06-Jun-1995 #text\_change 09-Jul-2004
C;Accession: S33733
R;Webb, T.B.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnsto PEBS Lett. 324, 219-225, 1993
R;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Residues: 1-362 <WEB>
A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395
C;Superfamily: ATP receptor P2u

C;Superfamily: ATP receptor P2u C;Keywords: G protein-coupled receptor; transmembrane protein

DB 2; Length 362;

Query Match

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heptahelical P2Y5-like receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 NVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLS
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                                                                                                                                     CVDPILYFLAGDTFRRRLSRATRK 330
                                                                                                                                                                   CFNPLLYYFAGENFKDRLKSALRK 322
                                                                                                                                                                                                           SIYLVIIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNS
                                                                                                                                                                                                                                           ALTTIIITLIIFFLCFLPYHTLRTVHL-----TTWKVGLCKDRLHKALVITLALAAANA
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                                                                                                                                                                                                                                                                                                                ----LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.3%; Score 470; DB 2; 30.6%; Pred. No. 6.1e-31;
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RESULT 3

150241

G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 0
C;Accession: I50241; JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced i
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 «KAP>
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN::
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:95190677; PMID:8819790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 «WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g
C;Comment: This receptor plays a role in T-cell activation.
C;Gene:tos:
A;Gene: p2Y5
C;Superimental source: T-cells
C;Comment: gransmembrane #status predicted <TM1>F;15-40/Domain: transmembrane #status predicted <TM2>F;89-109/Domain: transmembrane #status predicted <TM3>
F*99-109/Domain: transmembrane #status predicted <TM3>
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R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D. Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely: A;Reference number: JC5549; MUID:97366605; PMID:9223435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 <JAN>
A;Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g22
C;Superfamily: ATP receptor P2u
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Alternate names: purinoceptor 6H1
Salternate names: purinoceptor 6H1
Species: Gallus gallus (chicken)
Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
Accession: I50241; JC4618
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Pred. No. 4.2e-29;
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                                                                                                                                                                                                                                    PID: 9304384
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R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P. Biochem. Biophys. Res. Commun. 218, 793-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor. A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615; MUID:96158962; PMID:8579591
A;Molecule type: mRNA A;Residues: 1-373 cAYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: crythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Bescription: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Status: rraisara.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence revision 16-Aug-1996 #text_change 09-Jul-
C;Accession: JC4737; JC4615; \(\overline{S}\)4453
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.;
Biochem. Biophys. Res. Commun. 221, S88-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:Z49205;
                                                                                                                                                                                                                                                                                                                                               C;Comment: This receptor belongs
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: UNIPROT:P47900;
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F;177-201/Domain: transmembrane #status
F;227-248/Domain: transmembrane #status
F;269-292/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                        A;Gene: p2Y1; GDB:P2RY1
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of G protein-coupled receptors
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P2Y receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Apccies: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Blochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Hitle: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;MClecule type: mRNA
A;Residues: 1-373 <HRN
A;Cross-references: UNIPROT:948042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g
C;Genetics:
A;Gene: bovp2y
C;Genetics: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM3>
F;111-191/Domain: transmembrane #status predicted <TM3>
F;111-191/Domain: transmembrane #status predicted <TM5>
F;161-282/Domain: transmembrane #status predicted <TM7>
F;111-27/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
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TIENFKREFFFIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFN
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                                                       Score 442; DB 2; Length 373
Pred. No. 1.2e-28;
8; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 446; DB 2;
Pred. No. 5.7e-29;
9; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111;
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A;Cross-references: UNIPROT:P32249; GB:L08177; NID:g292056; PA;Experimental source: B-lymphocytes A;Note: sequence extracted from NCBI backbone (NCBIN:127096, C;Superfamily: ATP receptor P2u C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, J. Virol. 67, 2209-2220, 1993
J. Virol. 8, Pastein-Barr virus-induced genes: first lymphocyte-specific A;Reference number: A45680; MUID:93188173; PMID:8383238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: nucleic acid
A; Residues: 1-361 <BIR>
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                                                                                                                                                                 252 TLIIFFLCFLPYHTLRTVHLTTWKVGL-----CKDR--LHKALVITLALAAANACFNPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP 262
YFFACKGYKRKVMRMLKR
                                                     YYFAGENFKDRLKSALRK
                                                                                                              IIVVPVLCFTPYHVAIIQHMIK-KLRFSNFLECSQRHSFQISLHFTVCLMNFNCCMDPFI
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                                                                                                                                                                                                                                                                               KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE-----VPESGLRVSHRKALTTIII
                                                                                                                                                                                                                                                                                                                                        AVVHPLRYNKIKRIBHAKGVCIFVWILVFAQTLPLLINPMSKQEABRITCMEYPNFEETK 191
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Pred. No. 1.7e-28;
3; Mismatches 139
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PMID:8383238
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intron 17 purinergic receptor P2Y5 - human
N; Alternate names: G-protein coupled receptor
C; Species: Homo sapiens (man)
C; Apecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C; Accession: T09508
R; Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A; Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the
A; Reference number: Z16705
A; Accession: T09508
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Claession: T09508
A; Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:g2232068; PID:g2232069
C; Genetics:
A; Map position: 13
C; Superfamily: ATP receptor P2u
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                  RESULT 8

A47556

ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-i
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-517, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblast
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 < LUS
A;Cross-references: UNIPROT:P35383; GB:L14751; NID:g309457; PIDN:AAJ
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein
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Matches 106
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Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKTLRTKRNAKIVCTGVWLTVIGGSAPAVFVQSTHSQGNNASEACFE-NFPEATWKTYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLHVTSIRSAWILCGIIWILIM---ASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSRNCTI-ENEKREFFFIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFVFTLPFRI-FYFTTRNWPFGDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVYPFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSSHCFYNDSFKYTLYGCMFSMVFVLGLVSNCVAIYIFICVLKVRNETTTYMINLAMSDL
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                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
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| NGTFSNNN-SRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPY
                                                                             23.6%;
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Pred. No. 3.4e-28;
                                                                               Score 421.5;
Pred. No. 5.
                                                         Mismatches
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                                                                               .6e-27;
                                                                                               DB 2;
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                                                             131;
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                                                           Indels
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A;Title: Cloning by functional expression of platelet-activating factor receptor from g A;Reference number: $13638; MUID:91101726; PMID:1846231
A;Accession: $13638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-342 <HON>
A;Residues: 1-342 <HON>
A;Residues: 1-342 <HON>
A;Rosereferences: UNIPROT:P21556; GB:X56736; NID:949442; PIDN:CAA40060.1; PID:949443
A;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         platelet-activating factor receptor - guinea pig (,Species: Cavia porcellus (guinea pig) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 C;Accession: S13638 R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Wa
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Nature 349, 342-346, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                             RLLHVTSIRSAWILCGIIWILIM--ASSIMLLD-----SGSEQNGSVTSCLELNLYKIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                  NSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVNVFMLNLAISD
                                     DRLKSALRKGHPQKAKTKC
                                                                                                               LCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPLLYYFAGENFK 313
                                                                                                                                                                                              LOTMNYIALVVGCLLPFFTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF
                                                                                                                                                                                                                                                                                                                                         LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF
                                                                                                                                                                                                                                                                                                                                                                                                 NSSSRVDSEFRYTLFPIVYSIIFVLGIIANGYVLWVFARLYPSKKLNEIKIFMVNLTVAD
                                                                          ICFVPHHMVQ-LPWTLAELGMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFR
                                                                                                                                                       PVLIIHICIVLGFFIVFLLILFCNLVIIHTLLRQPVKQQRNAEVRRRALWMVCTVLAVFV
                                                                                                                                                                                                                                        KTAQATTRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNKAGSGNITRCFE-HYEKGSK
                                                                                                                                                                                                                                                                                                                    LLFLITLPLWIVYYSNQGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRAKRKSVRTIALVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAINMAYKITRPLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGL-CK--DRLHKALVITLALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHDTSARELFSHFVA-----YSSVMLGLLFAVPFSVILVCYVLMARRLLKPAYGTTGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSVTSCLELNLYKIAKLQTMNYIALVVGCL--LPFFTLSICYLLIIRVLLKVEV-PESGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLTCISVHRCLGVLRPLHSLRWGRARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTWNASTTYMFHLAVSDSLYAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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-NIMRSSQKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 416; DB 2;
Pred. No. 1.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137;
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RESULT 10 A54946 P-2U nucleotide

receptor

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A; rearr, C.B.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994

A; Title: Cloning and expression of a human P-2U nucleotide receptor, a target A; Reference number: A54946; MUID:94211846; PMID:8159738

A; Accession: A54946

A; Status: preliminary
A; Molecule type: mRNA; protein
A; Residues: 1-375 < PAR>
A; Cross - parts of this sequence were confirmed by protein semipancian C; Genetics:
                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text change 09-Jul-2004
C;Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text change 09-Jul-2004
C;Accession: A40191; JH0479; Ā41079; JC1359; A42831; I51923
R;Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A;Title: The human leukocyte platelet-activating factor receptor. cDNA clon
A;Reference number: A40191; MUID:92250505; PMID:1374385
A;Accession: A40191
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
A40191
platelet-activating factor receptor -
C;Species: Homo saplens (man)
C;Date: 28-Aug-1992 #sequence revision
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C;Date:
C;Access
R;Parr,
A;Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; A;Experimental source: granulocyte, cell line HL-60 all R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.
                                                                                       A; Accession: JH0479
A; Molecule type: mp.
                                                                                                                            A;Cross-references: UNIPROT:P25105; GB:M76674; NID:g456293; PIDN:AAA60002.1; R;Ye, R.D.; Prossnitz, B.R.; Zou, A.; Cochrane, C.G. Biochem. Blophys. Res. Commun. 180, 105-111, 1991
A;Title: Characterization of a human cDNA that encodes a functional receptor A;Reference number: JH0479; MUID:92028922; PMID:1656963
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A;Cross-references: GDB:362713;
A;Map position: 11q13.5-11q14.1
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled re
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A; Residues: 1-342 < KUN>
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                                                                     ;Molecule type: mRNA
;Residues: 1-342 <YER>
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Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 23.3%; Score 416; DB 2; Similarity 31.6%; Pred. No. 1.6e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFALCFLPFHVTRTLYYSFRSLDL---SCHTLNAINMAYKVTRLASANSCLDPVLYFLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGVLRPLRSLRWGRARYARRVAGAVWVLVLACQAPVLYFVTTSARGPLTCHDTSAPELFS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FHLAVSDALYAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGTESNNN-SRNCTI-BNEKRBEFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLA----LAAANACFNPLLYYFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RFVAYSSVMLGLLFAVPFAVILVCYVLMARRLLKPAYGTSGGLPRAKRKSVRTIAVVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQTMNYIALVVGCL--LPFFTLSICYLLIIRVLLKVEVPES-GLRVSHRKALTTIIITLI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGTWDGDELGYRCRFNEDFKYVLLÞVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 131,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 375;
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    H.; Minami,
                                         PID:g189538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                    cDNA cloning,
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    Bito,
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                                                                                                                                                                                                                       PID:g45629
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F;134-155/Domain: transmembrane #status predicted <TIV>
F;184-205/Domain: transmembrane #status predicted <TRV>
F;233-253/Domain: transmembrane #status predicted <TVI>
F;233-253/Domain: transmembrane #status predicted <TVI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: G protein-coupled receptor; transmembrane F;17-38/Domain: transmembrane #status predicted <TRI>F;54-75/Domain: transmembrane #status predicted <TII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-226,'TG',229-342 <SEY>
A;Residues: 1-226,'TG',229-342 <SEY>
A;Residues: 1-226,'TG', NID:g190697; PIDN:AAA60214.1; PID:g190698
A;Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R;Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for A;Reference number: IS1923; MUID:93192035; PMID:8383507
A;Accession: IS1923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: the authors translated the codon AAT for residue 316 R;Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976 R;Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Biochem. Biophys. Res. Commun. 189, 617-624, 1992 A;Title: Molecular cloning and characterization of the platelet-activating factor r. A;Reference number: JC1359; MUID:93112021; PMID:1281995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Molecular cloning and expression of platelet-activating A;Ritle: Molecular cloning and expression of platelet-activating A;Reference number: A41079; MUID:92041873; PMID:1657923 A;Accession: A41079 A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1p35-1p34.3
C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: PTAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-342 <RES>
A;Cross-references: GB:S56396; NID:g298580; PIDN:AAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-315,'N',317-342 < SUG:
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A; Residues: 1-342 <NAK>
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Best Local
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                                                                                                                                                                       188
                                                                                                                                                                                                                            114 NREQAVTRETKTAQANTRKRGISLSLVIWVAIVGAASYELILDSTNTVEDSAGSGNVTRC
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MVCTVLAVFIICFVPHHVVQ-LPWTLAELGFQDSKFHQAINDAHQVTLCLLSTNCVLDPV
                                                        TIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPL
                                                                                                                                                     LELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALT
                                                                                                                                                                                                                                                                                                                                     VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 134
                                                                                                                                                                                                                                                                                  VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDS-----GSEQNGSVTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN
                                                                                                           FE-HYEKGSVPVLIIHIFIVFSFFLVFLIILFCNLVIIRTLLMQPVQQQRNAEVKRRALW
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEPHDS-SHMDS-----EFRYTLFPIVYSIIFVLGVIANGYVLWVFARLYPCKKFNEIK
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platelet activating factor receptor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S63666
R;Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimi Biochem. J. 314, 671-678, 1996
A;Title: A murine platelet-activating factor receptor gene: cloning, chromos A;Reference number: S63666; MUID:96239129; PMID:8670084
A;Recession: S63666
A;Status: preliminary A;Accession: S63666
A;Status: preliminary A;Miniminary A;Minimina
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S63666
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Residues: 1-420 <GER>
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                                                                                                                              Similarity
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MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTQKIPRLDITTCHDVLDLKDLKDEYIYYFSSF--CLLFFFVPFIITTICYIGIIRSLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSIENS----CKKTRALFLAVVVLCVFIICFGPTNVLFLTHY----LQEANEFLYFAYILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ---NGSVTSCLELNLYKIAKLQTMNYIALVVGCLL----PFFTLSICYLLIIRVLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAIIIFLFKMKVRKPAVVYMLNLAIADVFFVSVLPFKIAYHLSGNDWLFGPGMCRIVTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELDESGEGSGDQAPVSRSARKPIRRNITKEAEQYLSSQWLTKFVPSLYTVVFIVGLPLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMEPHGTFSHNNS------RNCTIE-----NFKREFFPIVYLIIFFWGVLGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYYFAGENFKDRLKSALRKGHPQKAKTKC
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                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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30.9%;
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                                                                                                  66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                            Score 404; DB 2; L
Pred. No. 1.4e-25;
6; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 406; DB 2;
Pred. No. 1.2e-25;
6; Mismatches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                 EMBL: D50872; NID: g1256924; PIDN: BAA09468.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
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                                                                                                                                                  Length 341,
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                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T.; Shimizu,
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A,Residues: 1-137,'A','139-397 <BOE>
A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
A;Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A;Reference number: H00822
A;Reference number: H00822
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; PID:g1208540
C;Genetics:
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                                                                                                                                                                                                                                                                                             A;Map position: 5q13
A;Introns: 28/1
C;Superfamily: ATP receptor P2u
C;Superfamily: ATP receptor P2u
F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:g1008084; PIDN:CAA90290.1; PID:g100 R;Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn Biochem. J. 314, 1009-1016, 1936
Biochem. J. 314, 1009-1016, 1958
A;Title: Molecular cloning, expression and potential functions of the human proteinase-a A;Reference number: S64709; MUID:96177879; PMID:8615752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteinase-activated receptor 2 precursor - human C;Species: Homo sapiens (man) C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 C;Accession: S66518; S64709; G02131 R;Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroemb Eur. J. Biochem. 232, 84-89, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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A; Residues: 1-397 < NYS>
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Best Local (
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                                                                                                                        FFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYL 99
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                                                               FLPIVYTIVFVVGLPSNGMALWVFLFRTKKKHPAVIYMANLALADLLSVIWFPLKIAYHI
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                                                                                                                                                                                    Conservative
                                                                                                                                                                                                              22.4%;
                                                                                                                                                                                        69;
                                                                                                                                                                              Score 400.5; DB 2
Pred. No. 3.1e-25;
9; Mismatches 121
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                                                                                                                                                                                                                                          DB 2;
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angiotensin receptor homolog APJ - human C;Species: Homo sapiens (man) c;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004 C;Accession: 138435 R;O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr Gene 136, 355-360, 1993 Gene 136, 355-360, 1993 A;Title: A human gene that shows identity with the gene encoding the angiotensin recepto A;Reference number: 138435; MUID:94124031; PMID:8294032 A;Accession: 138435
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I38435
Search completed: December 13, 2004, 17:53:20 Job time : 42 secs
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A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-380 <RES>
Cross-references: UNIPROT:P35414; EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                                                                                                                                                             290 --TLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKT 330
                                                                                                                                                                               239 ---GLR-KRRRLLSIIVVLVVTFALCMMPYHLVKTLYMLGSLLHWP----CDFDLFLMNIF 291
                                                                                                                                                                                                                             234
                                                                                                                                                                                                                                                                      181 CY-MDYSMVATVSSEWAWEVGLGVSSTTVGFVVPFTIMLTCYFFIAQTIAGHFRKERIE-
                                                                                                                                                                                                                                                                                                                      187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 NLLLVVHYFLIK-SQGQSHVYALYIVALCLSTLNSCIDFFYYYFVSHDFRDHAKNALL-- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 SLAIGVFLFPAFLTASAYVLMIRMLRSSAMDENSEK-KRKRAIKLIVTVLAMYLICFTPS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 ALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLPY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 - CRSVRTVKQMQVSLTSKKHSR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 HPQKAKTKCVFPVSVWLRKETR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 HTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRSADIFIASLAVADLTEVVTLELWATYTYRDYDWPFGTFFCKLSSYLIFVNNYASVFCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 MEDNGTFSN----NNSRNCTIENFKRE--FFPIVYLIIFFWGVLGNGLSIY-VFLQPYKK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 STSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 129
                                                                                                                                                                                                                      PESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVH----LTTWKVGLCKDRLHKALVI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GISLAIWLLILLVTIPLYVVKQTIFIPAL-----NITTCHDVLPEQLLVGDMFNYFL 244
                                                                                                                                                                                                                                                                                                                    CLELNLYKIAKLQT------MNYIALVVGCLLPFFTLSICYLLIIRVLL------KVEV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI---IWILIMASSIML------LDSGSEQNGSVTSCLELNLYKIAKLQTMNY-I 204
                                                                                      PYCTCISYVNSCLNPFLYAFFDPRFRQACTSMLCCGQSRCAGT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEEGGDFDNYYGADNQSECEYTDWKSSGALIPAIYMLVFLLGTTGNGLVLWTVFRSSREK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                         238
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